



FIG. 1A

Frame 2

ATG	CAT	GGA	GTG	GAC	CTG	TAG	GCG	ACT	TGC	ATC	GTC	TTC	AAC	M	K	I	A
		10			19			28			37			46	46	46	55

HF 6479

T	V	S	V	L	L	P	L	A	L	C	L	I	Q	D	A	A	S	K	N
ACA	GTG	TCA	GTG	CTT	CTG	CCC	TTG	GCT	CTT	TGC	CTC	ATA	CAA	GAT	GCT	GCC	AGT	AAG	AAT
		64			73			82			91			100			109		

Repeat 1

E	D	Q	E	M	C	H	E	F	Q	A	F	M	K	N	G	K	L	F	C
GAA	GAT	CAG	GAA	ATG	TGC	CAT	GAA	TTT	CAG	GCA	TTT	ATG	AAA	AAT	GGA	AAA	CTG	TTC	TGT
		124			133			142			151			160			169		

HF 6479

P	Q	D	K	K	F	F	Q	S	L	D	G	I	M	F	I	N	K	C	A
CCC	CAG	GAT	AAG	AAA	TTT	TTT	CAA	AGT	CTT	GAT	GGA	ATA	ATG	TTC	ATC	AAT	AAA	TGT	GCC
		184			193			202			211			220			229		

typical Kazal domain 1

R	A	P	K	A	T	A	P	T	E	L	N	C	D	D	F	K	K	G	E
AGA	GCT	CCC	AAG	GCT	ACT	GCC	CCA	ACA	GAG	CTG	AAT	TGT	GAT	GAT	TTT	AAA	AAA	GGA	GAA
		304			313			322			331			340			349		

Repeat 2

V	K	S	E	G	E	C	K	S	S	N	P	E	Q	D	V	C	S	A	F
GTA	AAA	AGT	GAA	GGG	GAA	TGT	AAG	AGC	AGT	AAT	CCA	GAG	CAG	GAT	GTA	TGC	AGT	GCT	TTT
		484			493			502			511			520			529		

Repeat 3

C	K	E	Y	E	K	Q	V	R	N	G	R	L	F	C	T	R	E	S	D
TGC	AAG	GAA	TAT	GAA	AAA	CAA	GTG	AGA	AAT	GGA	AGG	CTT	TTT	TGT	ACA	CGG	GAG	AGT	GAT
		724			733			742			751			760			769		

Repeat 4

E	K	T	K	V	K	R	E	I	V	K	L	C	S	Q	Y	Q	N	Q	A
GAA	AAA	ACT	AAA	GTT	AAA	AGA	GAA	ATT	GTG	AAA	CTC	TGC	AGT	CAA	TAT	CAA	AAT	CAG	GCA
		904			913			922			931			940			949		



# FIG. 1B

#  
K N G I L F C T R E N D P I R G P D G K  
AAG AAT GGA ATA CTT TTC TGT ACC AGA GAA AAT GAC CCT ATT CGT GGT CCA GAT GGG AAA  
964 973 982 991 1000 1009

# \*  
M H G N L C S M C Q V Y F Q A E N E E K  
ATG CAT GGC AAC TTG TGT TCC ATG TGT CAA GTC TAC TTC CAA GCA GAA AAT GAA GAA AAG  
1024 1033 1042 1051 1060 1069

—> HF 7665  
K K A E A R A R N K R E S G K A T S Y A  
AAA AAG GCT GAA GCA CGA GCT AGA AAC AAA AGA GAA TCT GGA AAA GCA ACC TCA TAT GCA  
1084 1093 1102 1111 1120 1129

## Repeat 5

\* #  
E L C N E Y R K L V R N G K L A C T R E  
GAG CTT TGC AAT GAA TAT CGA AAG CTT GTG AGG AAC GGA AAA CTT GCT TGC ACC AGA GAG  
1144 1153 1162 1171 1180 1189

# \*  
N D P I Q G P D G K V H G N T C S M C E  
AAC GAT CCT ATC CAG GGC CCA GAT GGG AAA GTG CAC GGC AAC ACC TGC TCC ATG TGT GAG  
1204 1213 1222 1231 1240 1249

HF 7665 <—  
V F F Q A E E E E K K K K E G E S R N K  
GTC TTC TTC CAA GCA GAA GAA GAA GAA AAG AAA AAG GAA GGC GAA TCA AGA AAC AAA  
1264 1273 1282 1291 1300 1309

## Repeat 6

\* #  
R Q S K S T A S F E E L C S E Y R K S R  
AGA CAA TCT AAG AGT ACA GCT TCC TTT GAG GAG TTT TGT AGT GAA TAC CGC AAA TCC AGG  
1324 1333 1342 1351 1360 1369

# \*  
K N G R L F C T R E N D P I Q G P D G K  
AAA AAC GGA CGG CTT TTT TGC ACC AGA GAG AAT GAC CCC ATC CAG GGC CCA GAT GGG AAA  
1384 1393 1402 1411 1420 1429

# \*  
M H G N T C S M C E A F F Q Q E E R A R  
ATG CAT GGC AAC ACC TGC TCC ATG TGT GAG GCC TTC TTT CAA CAA GAA GAA AGA GCA AGA  
1444 1453 1462 1471 1480 1489

## Repeat 7

\* #  
A K A K R E A A K E I C S E F R D Q V R  
GCA AAG GCT AAA AGA GAA GCT GCA AAG GAA ATC TGC AGT GAA TTT CGG GAC CAA GTG AGG  
1504 1513 1522 1531 1540 1549

# \*  
N G T L I C T R E H N P V R G P D G K M  
AAT GGA ACA CTT ATA TGC ACC AGG GAG CAT AAT CCT GTC CGT GGA CCA GAT GGC AAA ATG  
1564 1573 1582 1591 1600 1609

# \*  
H G N K C A M C A S V F K L E E E E K K  
CAT GGA AAC AAG TGT GCC ATG TGT GCC AGT GTG TTC AAA CTT GAA GAA GAA GAG AAG AAA  
1624 1633 1642 1651 1660 1669

N D K E E K G K V E A E K V K R E A V Q  
AAT GAT AAA GAA GAA AAA GGG AAA GTT GAG GCT GAA AAA GTT AAG AGA GAA GCA GTT CAG  
1684 1693 1702 1711 1720 1729

## Repeat 8

\* #  
E L C S E Y R H Y V R N G R L P C T R E  
GAG CTG TGC AGT GAA TAT CGT CAT TAT TAT GTG AGG AAT GGA CGA CTC CCC TGT ACC AGA GAG  
1744 1753 1762 1771 1780 1789

# \*  
N D P I E G L D G K I H G N T C S M C E  
AAT GAT CCT ATT GAG GGT CTA GAT GGG AAA ATC CAC GGC AAC ACC TGC TCC ATG TGT GAA  
1804 1813 1822 1831 1840 1849

A F F Q Q E A K E K E R A E P R A K V K  
GCC TTC TTC CAG CAA GAA GCA AAA GAA GAA GAA GCT GAA CCC AGA GCA AAA GTC AAA  
1864 1873 1882 1891 1900 1909

## Repeat 9

\*  
R E A E K E T C D E F R R L L Q N G K L



FIG. 1C

AGA GAA GCT GAA AAG GAG ACA TGC GAT GAA TTT CGG AGA CTT TTG CAA AAT GGA AAA CTT  
1924 1933 1942 1951 1960 1969  
#  
F C T R E N D P V R G P D G K T H G N K  
TTC TGC ACA AGA GAA AAT GAT CCT GTG CGT GGC CCA GAT GGC AAG ACC CAT GGC AAC AAG  
1984 1993 2002 2011 2020 2029  
#  
C A M C K A V F Q K E N E E R K R K E E  
TGT GCC ATG TGT AAG GCA GTC TTC CAG AAA GAA AAT GAG GAA AGA AAG AGG AAA GAA GAG  
2044 2053 2062 2071 2080 2089

E D Q R N A A G H G S S G G G G G N T Q  
GAA GAT CAG AGA AAT GCT GCA GGA CAT GGT TCC AGT GGT GGT GGA GGA GGA AAC ACT CAG  
2104 2113 2122 2131 2140 2149

Repeat 10

\*  
D E C A E Y Q E Q M K N G R L S C T R E  
GAC GAA TGT GCT GAG TAT CAG GAA CAA ATG AAA AAT GGA AGA CTC AGC TGT ACT CGG GAG  
2164 2173 2182 2191 2200 2209  
#  
S D P V R D A D G K S Y N N Q C T M C K  
AGT GAT CCT GTA CGT GAT GCT GAT GGC AAA TCG TAC AAC AAT CAG TGT ACC ATG TGT AAA  
2224 2233 2242 2251 2260 2269  
#  
A K L E R E A E R K N E Y S R S R S N G  
GCA AAA TTG GAA AGA GAA GCA GAG AGA AAA AAT GAG TAT TCT CGC TCC AGA TCA AAT GGG  
2284 2293 2302 2311 2320 2329

Repeat 11

\*  
T G S E S G K D T C D E F R S Q M K N G  
ACT GGA TCA GAA TCA GGG AAG GAT ACA TGT GAT GAG TTT AGA AGC CAA ATG AAA AAT GGA  
2344 2353 2362 2371 2380 2389  
#  
K L I C T R E S D P V R G P D G K T H G  
AAA CTT ATC TGC ACT CGA GAA AGT GAC CCT GTC CGG GGT CCA GAT GGC AAG ACA CAT GGT  
2404 2413 2422 2431 2440 2449  
#  
N K C T M C K E K L E R E A A E K K K K  
AAT AAG TGT ACT ATG TGT AAG GAA AAA CTG GAA AGG GAA GCA GCT GAA AAA AAA AAG AAA  
2464 2473 2482 2491 2500 2509  
#  
E D E D R S N T G E R S N T G E R S N D  
GAG GAT GAA GAC AGG AGC AAT ACA GGA GAA AGG AGC AAT ACA GGA GAA AGG AGC AAT GAC  
2524 2533 2542 2551 2560 2569

Repeat 12

\*  
K E D L C R E F R S M Q R N G K L I C T  
AAA GAG GAT CTG TGT CGT GAA TTT CGA AGC ATG CAG AGA AAT GGA AAG CTT ATC TGC ACC  
2584 2593 2602 2611 2620 2629  
#  
R E N N P V R G P Y G K M H I N K C A M  
AGA GAA AAT AAC CCT GTT CGA GGC CCA TAT GGC AAG ATG CAC ATC AAT AAA TGT GCT ATG  
2644 2653 2662 2671 2680 2689  
#  
C Q S I F D R E A N E R K K K D E E K S  
TGT CAG AGC ATC TTT GAT CGA GAA GCT AAT GAA AGA AAA AAG AAA GAT GAA GAG AAA TCA  
2704 2713 2722 2731 2740 2749

Repeat 13

\*  
S S K P S N N A K D E C S E F R N Y I R  
AGT AGC AAG CCC TCA AAT AAT GCA AAG GAT GAG TGC AGT GAA TTT CGA AAC TAT ATA AGG  
2764 2773 2782 2791 2800 2809  
#  
N N E L I C P R E N D P V H G A D G K F  
AAC AAT GAA CTC ATC TGC CCT AGA GAG AAT GAC CCA GTG CAC GGT GCT GAT GGA AAG TTC  
2824 2833 2842 2851 2860 2869  
#  
Y T N K C Y M C R A V F L T E A L E R A  
TAT ACA AAC AAG TGC TAC ATG TGC AGA GCT GTC TTT CTA ACA GAA GCT TTG GAA AGG GCA  
2884 2893 2902 2911 2920 2929  
#  
K L Q E K P S H V R A S Q E E D S P D S  
AAG CTT CAA GAA AAG CCA TCC CAT GTT AGA GCT TCT CAA GAG GAA GAC AGC CCA GAC TCT  
2944 2953 2962 2971 2980 2989



FIG. 1D

F	S	S	L	D	S	E	M	C	K	D	Y	R	V	L	P	R	I	G	Y				
TTC	AGT	TCT	CTG	GAT	TCT	GAG	ATG	TGC	AAA	GAC	TAC	CGA	GTA	TTG	CCC	AGG	ATA	GGC	TAT				
3004				3013				3022				3031				3040				3049			
#								+								!							
L	C	P	K	D	L	K	P	V	C	G	D	D	G	Q	T	Y	N	N	P				
CTT	TGT	CCA	AAG	GAT	TTA	AAG	CCT	GTC	TGT	GGT	GAC	GAT	GGC	CAA	ACC	TAC	AAC	AAT	CCT				
3064				3073				3082				3091				3100				3109			
#				*																			
C	M	L	C	H	E	N	L	I	R	Q	T	N	T	H	I	R	S	T	G				
TGC	ATG	CTC	TGT	CAT	GAA	AAC	CTG	ATA	CGC	CAA	ACA	AAT	ACA	CAC	ATC	CGC	AGT	ACA	GGG				
3124				3133				3142				3151				3160				3169			
+																							
K	C	E	E	S	S	T	P	G	T	T	A	A	S	M	P	P	S	D	E				
AAG	TGT	GAG	GAG	AGC	AGC	ACC	CCA	GGA	ACC	ACC	GCA	GCC	AGC	ATG	CCC	CCG	TCT	GAC	GAA				
3184				3193				3202				3211				3220				3229			
TGA	CAG	GAA	GAT	TGT	TGA	AAG	CCA	TGA	GGG	AAA	AAA	TAA	ACC	CCA	GTT	CTG	AAT	CAC	CTA				
3244				3253				3262				3271				3280				3289			
CCT	TCA	CCA	TCT	GTA	TAT	ACA	AAG	AAT	TCT	TCG	GAG	CTT	GTC	TTA	TTT	GCT	ATA	GAA	AAC				
3304				3313				3322				3331				3340				3349			
AAT	ACA	GAG	CTT	TTG	GGA	ATG	GAA	TCA	CTG	ATT	TTC	AGT	CTT	TTC	CAT	TTC	TTT	CCT	CCT				
3364				3373				3382				3391				3400				3409			
AGA	ATC	TGT	GAT	CTG	AGG	GTA	TAA	AGA	CAT	TTC	CAC	CAA	GTT	TGA	GCC	CTC	AAA	ATG	TCC				
3424				3433				3442				3451				3460				3469			
polyadenylation signal																							
TGA	TTA	CAA	TGC	TGT	CTG	TCC	AAC	TGC	CTG	TTC	AAT	AAA	AGT	AAA	CTC	AGC	AGA	AAA...					
3484				3493				3502				3511				3520				3529			

.....poly(A) tail

The following sequence corrections have been performed:

An additional A in position 2510 results in a frame shift which produces three additional inhibitor domains.

Base were exchanged in ten different positions:

Position 551: G for A  
Position 1207: C for T  
Position 1258: C for T  
Position 1261: C for T  
Position 2175: A for G  
Position 2950: G for A  
Position 3228: C for T  
Position 3284: C for T  
Position 3324: C for T  
Position 3337: C for T

SEQUENZPROTOKOLL

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